

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/383,745

DATE: 05/04/2001

TIME: 12:39:12

Input Set : N:\Crf3\RULE60\09383745.txt

Output Set: N:\CRF3\05042001\I383745.raw

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74          260          265          270
76 Val Leu Asp Glu Phe Lys Met Glu Lys Arg Ile Ser Arg Met Phe Tyr
77          275          280          285
79 Ile Met Thr Phe Leu Phe Leu Thr Leu Trp Gly Pro Tyr Leu Val Ala
80          290          295          300
82 Cys Tyr Trp Arg Val Phe Ala Arg Gly Pro Val Val Pro Gly Gly Phe
83 305          310          315          320
85 Leu Thr Ala Ala Val Trp Met Ser Phe Ala Gln Ala Gly Ile Asn Pro
86          325          330          335
88 Phe Val Cys Ile Phe Ser Asn Arg Glu Leu Arg Arg Cys Phe Ser Thr
89          340          345          350
91 Thr Leu Leu Tyr Cys Arg Lys Ser Arg Leu Pro Arg Glu Pro Tyr Cys
92          355          360          365
94 Val Ile
95          370
98 <210> SEQ ID NO: 2
99 <211> LENGTH: 2810
100 <212> TYPE: DNA
101 <213> ORGANISM: Homo sapiens
103 <220> FEATURE:
104 <221> NAME/KEY: misc_feature
105 <222> LOCATION: (1)..(2810)
106 <223> OTHER INFORMATION: n= a, g, c or t
108 <400> SEQUENCE: 2
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110 cttactgaga gctccatttc tggaaagcct tacaagactg aggaatatca gactgcgaat 120
111 caccgggaac ggttcctttg cagcacagaa gcaatctctc tccccatctt cgcataattct 180
112 aatggcaaaa caagtggaag aaaagaggaa gcatgactgc agatcagatc agttctcttt 240
113 gtggattata ttttcagtaa aatgtatgga tctatctttt ccttggttctt atatctagat 300
114 catgagactt gactgaggct gtatccttat cctccatcca tctatggcga actatagcca 360
115 tgcagctgac aacattttgc aaaatctctc gcctctaaca gcctttctga aactgacttc 420
116 cttgggtttc ataataggag tcagcgtggt gggcaacctc ctgatctcca ttttgctagt 480
117 gaaagataag accttgcata gagcacctta ctacttctctg ttggatcttt gctgttcaga 540
118 tctcctcaga tctgcaattt gtttccattt tgtgttcaac tctgtcaaaa atggctctac 600
119 ctggacttat gggactctga cttgcaaagt gattgccttt ctgggggttt tgcctctgtt 660
120 ccacactgct ttcattgctt tctgcatcag tctcaccaga tacttagcta tcgccccatca 720
121 ccgcttctat acaaagaggg tgaccttttg gacgtgtctg gctgtgatct gtatgggtgtg 780
122 gactctgtct gtggccatgg catttcccc ggtttttagac gtgggcactt actcattcat 840
123 tagggaggaa gatcaatgca cttccaaca ccgctccttc agggctaatt attccttagg 900
124 atttatgctg cttctgtctc tcctcctcct agccacacag cttgtctacc tcaagctgat 960
125 atttttcgtc cacgatcgaa gaaaaatgaa gccagtccag tttgtagcag cagtcagcca 1020
126 gaactggact tttcatggtc ctggagccag tggccaggca gctgccaat ggctagcagg 1080
127 atttggaagg ggtcccacac caccacctt gctgggcac aggcataatg caaacaccac 1140
128 aggcagaaga aggtatttgg tcttagacga gttcaaaatg gagaaaagaa tcagcagaat 1200
129 gttctatata atgacttttc tgtttctaac cttgtggggc ccctacctgg tggcctgtta 1260
130 ttggagagtt tttgcaagag ggcctgtagt accaggggga tttctaacag ctgctgtctg 1320
131 gatgagtttt gcccaagcag gaatcaatcc ttttgtctgc attttctcaa acagggagct 1380
132 gaggcgctgt ttcagcaca cccttcttta ctgcagaaaa tccaggttac caagggaacc 1440
133 ttactgtggt atatgagggg gcatctgtaa atctttagcc ttgtgaaaac taaccttctc 1500

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134 tgetgagcaa ttgtggccca tagccatatt ttgagaagaa attcaagaat ggaatcagca 1560
135 gttttaagga ttitgggcaac attctgcagt ctttgcaata gttcacctat aatcctattt 1620
136 taaatctcag agtgatcctg ctgactgcca gcaaagggtt gtaattaaga agggactgaa 1680
137 ccaactgccct aagtttcttt atgtggtcaa aaactagata atgaaagtag cagggtgctaa 1740
138 gtatcagtgc taaatgctct gtatgtcact acatatgaaa aaacatcaaa aaacaattag 1800
139 cattggacat cttataaat taagtigaca tgaggtaaatt gtgttgataa aaactaattt 1860
140 tagaagtttg aagactttaa aacatttcat actactattg ttttgcaaag actaaaatat 1920
141 ttggggactt aaagtactgt aatccactaa agacgtgcca atgaattatt ggaatatcac 1980
142 acttttaaaa ccgccttgta agttctggg agcattccaa agcagtatat tggttccaat 2040
143 tagagtttac tttttttgta ttaatacatt gctatttcta aataccactt tctcatcta 2100
144 ctagtaagat tgctagcatt gaactgtatt atgtggtttt tgttgatttg gtataaagtt 2160
145 tttccaattc atttatattt tacaaatgct agatattggt ctgggaggca acattaatgg 2220
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147 gggttatcta gkatccytc atcttattag cactggagca aatagycaag ggaaatcraa 2340
148 tcagtaactg gtcatggtca tgcacttraa agtgcattga agatcattta gtactttttc 2400
149 cttttttctc acatggttg aaacttaaag tgcacatcmc tgaataatg agattttctt 2460
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151 ttttaagtca gctgtcgagg ggagaccaca gccttagtat gacatcctgc acaattttgtg 2580
152 aagcatttat tctactgaag gcacagtctt gtttatactt tctgcacatt cagtgtattg 2640
153 gtcatttaaa ttatttcagt tttaacttgt gaaagcttat aatatgattt ctgggtattt 2700
W--> 154 agaaatacat tagagtctgt gagtctcatt ctttaagata canatgtgtg aacttcaata 2760
155 taaagttgca ttitgcaaaa tttaaaaaaa aaaaaaaaaa aaaaaaaaaa 2810
158 <210> SEQ ID NO: 3
159 <211> LENGTH: 269
160 <212> TYPE: PRT
161 <213> ORGANISM: Unknown
163 <220> FEATURE:
164 <223> OTHER INFORMATION: Description of Unknown Organism:Transmembrane
165 Receptor of the Rhodopsin Superfamily
167 <400> SEQUENCE: 3
168 Gly Asn Ile Leu Val Ile Trp Val Ile Cys Arg Tyr Arg Arg Met Arg
169 1 5 10 15
171 Thr Pro Met Asn Tyr Phe Ile Val Asn Leu Ala Val Ala Asp Leu Leu
172 20 25 30
174 Phe Ser Leu Phe Thr Met Pro Phe Trp Met Val Tyr Tyr Val Met Gly
175 35 40 45
177 Gly Arg Trp Pro Phe Gly Asp Phe Met Cys Arg Ile Trp Met Tyr Phe
178 50 55 60
180 Asp Tyr Met Asn Met Tyr Ala Ser Ile Phe Phe Leu Thr Cys Ile Ser
181 65 70 75 80
183 Ile Asp Arg Tyr Leu Trp Ala Ile Cys His Pro Met Arg Tyr Met Arg
184 85 90 95
186 Trp Met Thr Pro Arg His Arg Ala Trp Val Met Ile Ile Ile Ile Trp
187 100 105 110
189 Val Met Ser Phe Leu Ile Ser Met Pro Pro Phe Leu Met Phe Arg Trp
190 115 120 125
192 Ser Thr Tyr Arg Asp Glu Asn Glu Trp Asn Met Thr Trp Cys Met Ile
193 130 135 140
195 Tyr Asp Trp Pro Glu Trp Met Trp Arg Trp Tyr Val Ile Leu Met Thr

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196 145          150          155          160
198 Ile Ile Met Gly Phe Tyr Ile Pro Met Ile Ile Met Leu Phe Cys Tyr
199          165          170          175
201 Trp Arg Ile Tyr Arg Ile Ala Arg Leu Trp Met Arg Met Ile Pro Ser
202          180          185          190
204 Trp Gln Arg Arg Arg Arg Met Ser Met Arg Arg Glu Arg Arg Ile Val
205          195          200          205
207 Lys Met Leu Ile Ile Ile Met Val Val Phe Ile Ile Cys Trp Leu Pro
208          210          215          220
210 Tyr Phe Ile Val Met Phe Met Asp Thr Leu Met Met Trp Trp Phe Cys
211 225          230          235          240
213 Glu Phe Cys Ile Trp Arg Arg Leu Trp Met Tyr Ile Phe Glu Trp Leu
214          245          250          255
216 Ala Tyr Val Asn Cys Pro Cys Ile Asn Pro Ile Ile Tyr
217          260          265

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VERIFICATION SUMMARY

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L:154 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2